	08/6/2, 929 CRF Processing Date: 3/6/9 Edited by:
Changed	a file from non-ASCII to ASCII
Changed	the margins in cases where the sequence text was "wrapped" down to the next line.
Edited a f	ormat error in the Current Application Data section, specifically:
applicant	Current Application Data section with the actual current number. The number inputted by the was \text{\text{The prior application data; or } other \text{\text{other}}
Added the	e mandatory heading and subheadings for "Current Application Data".
Edited the	"Number of Sequences" field. The applicant spelled out a number instead of using an integer
Changed	the spelling of a mandatory field (the headings or subheadings), specifically:
Corrected	the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
nserted o	r corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
	subheading placement. All responses must be on the same line as each subheading. If the placed a response below the subheading, this was moved to its appropriate place.
nserted (colons after headings/subheadings. Headings edited included:
Deleted 6	extra, invalid, headings used by an applicant, specifically:
Deleted:	non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of numbers throughout text; other invalid text, such as
Inserted	mandatory headings, specifically:
	d an obvious error in the response, specifically:
Correcte	
	entifiers where upper case is used but lower case is required, or vice versa.
Edited id	
Edited id	entifiers where upper case is used but lower case is required, or vice versa.
Edited id Correcte A *Hard	entifiers where upper case is used but lower case is required, or vice versa. d an error in the Number of Sequences field, specifically:

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING PATENT APPLICATION US/08/612,929

DATE: 03/06/97

INPUT SET: S15989.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

```
Does Not Comply
                                                          Diskette Needed
 1
                                       SEQUENCE LISTING
 2
 3
    (1)
            General Information:
 4
 5
          (i) APPLICANT: Holmes, Stephen D.
                         Gross, Mitchell S.
 6
 7
                         Sylvester, Daniel R.
 8
         (ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
 9
10
                 Treatment of IL4 Mediated Disorders
11
12
        (iii) NUMBER OF SEQUENCES: 58
13
14
         (iv) CORRESPONDENCE ADDRESS:
15
               (A) ADDRESSEE: SmithKline Beecham Corporation
16
               (B) STREET: Corporate Intellectual Property, UW2220 - 709
17
                      Swedeland Rd.
               (C) CITY: King of Prussia
18
19
               (D) STATE: PA
20
               (E) COUNTRY: USA
21
               (F) ZIP: 19406-2799
22
23
         (v) COMPUTER READABLE FORM:
               (A) MEDIUM TYPE: Floppy disk
24
25
               (B) COMPUTER: IBM PC compatible
               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26
27
               (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28
29
         (vi) CURRENT APPLICATION DATA:
30
               (A) APPLICATION NUMBER: US 08/117,366
31
               (B) FILING DATE: 07-SEP-1994
               (C) CLASSIFICATION:
32
33
34
               (A) APPLICATION NUMBER: US 08/136,783
35
               (B) FILING DATE: 14-OCT-1993
36
               (C) CLASSIFICATION:
37
38
       (viii) ATTORNEY/AGENT INFORMATION:
39
               (A) NAME: Sutton, Jeffrey A.
40
               (B) REGISTRATION NUMBER: 34,028
41
               (C) REFERENCE/DOCKET NUMBER: P50186-2
42
43
        (ix) TELECOMMUNICATION INFORMATION:
44
               (A) TELEPHONE: (215) 270-5024
45
               (B) TELEFAX: (215) 270-5090
46
```

PAGE: 2

47

RAW SEQUENCE LISTING PATENT APPLICATION US/08/612,929

DATE: 03/06/97 TIME: 16:01:06

(2) INFORMATION FOR SEQ ID NO:1: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 396 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ii) MOLECULE TYPE: cDNA (ii) MOLECULE TYPE: cDNA (ii) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1396 (xi) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1396 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTC TGG GTT CCA ART GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTC TGG GTT CCA ART GAG ACA GAC ACA ATC TGG CTA TGG GTG CTG CTC TGG GTT CCA ART GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT TCC GCT TGG CTG (I) SET THT GLY ASP IHE Val Leu Thr Gln Ser Pro Ala Ser Leu Ala GCT TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC ACC CAA AGT Val Ser Leu Gly Gln Arg Ala Thr 11e Ser Cys Lys Ala Ser Gln Ser (I) SEQUENCE DESCRIPTION: SEQ ID NO:1: ACT GTT GTT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC ACC CAA AGT (I) MET CTT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC ACC CAA AGT (I) MET CTT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC ACC CAA AGT (I) Val Ser Leu Gly Gln Arg Ala Thr 11e Ser Cys Lys Ala Ser Gln Ser (I) Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro (I) Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro (I) GGG ATC CCA GCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT (I) Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser (I) GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC ATC TCC (I) GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC (I) Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser (I) GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC (I) Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser (I) GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC ACC TTA TCC (I) GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC (I) Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ala Thr Tyr Tyr Cys (I) GGG ATC CCA GCA AGT TT AGT GGC AGT TCC GGT GGG AGC ACC AAC CTG (I) Gln	4 /																	
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Signature Capacitic Capa			(i)) SE	QUEN	CE CI	HARA	CTER	ISTI	cs:								
C STRANDEDNESS: double (D) TOPOLOGY: unknown (52		•	(2	A) LI	ENGTI	H: 39	96 ba	ase j	pairs	5							
ST	53			(1	B) T	YPE:	nuc:	leic	aci	đ								
(ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1396 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	54			((C) S	rrani	DEDNI	ESS:	doul	ble								
(ii) MOLECULE TYPE: cDNA				(1	D) T(OPOL	OGY:	unkı	nown									
58																		
Carr			(ii) MOI	LECUI	LE T	YPE:	CDN	4									
60 (A) NAME/KEY: CDS 61 (B) LOCATION: 1396 62 63 64 65 66 67 68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 69 70 ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA 71 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro 72 1 5 10 15 73 74 GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT 75 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Scr Leu Ala 76 20 25 30 77 78 GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AAC CAA AGT 79 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser 80 35 40 45 81 82 GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA 83 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 84 50 55 85 GGA CAG CCA CAC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT 88 GGA CAG CCA CCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT 89 GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCC AAT CTA GAA TCT 80 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 80 GJ GIG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCC GGA ACC TCT ACC 81 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 80 GJ GAT C CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACC AGC TTC ACC 81 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr 85 90 86 GCA CAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT 87 GLU Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys 86 CCC AAC CAA AGT AAT GAG GAT CCT CCC ACC TTC GGT GGA GCC ACC AAC CTG 87 GLU Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys 88 CAG CAA AGT AAT GAG GAT CCT CCC ACG TTC CCG ACC TTC GGT GGA GCC ACC AAC CTG 89 CCC CAA AGT AAT GAG GAT CCT CCC ACG TTC CCG ACC TTC GGT GGA GCC ACC AAC CTG 80 GAG CAA AGT AAT GAG GAT CCT CCG ACC TTC GGT GGA GCC ACC AAC CTG 81 GLU Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys 80 CAG CAA AGT AAT GAG GAT CCT CCG ACC TTC CGT GGT GGA GCC ACC ACC ACC ACC TTC 80 CCC CAA AGT AAT GAG GAT CCT CCG ACC TTC CGT GGT GGA GCC ACC ACC ACC ACC TTC 81 CCC CAA AGT AAT GAG GAT CCT CCG ACC TTC CGT GGA GGC ACC ACC ACC ACC ACC TTC 81 CCC CAA AGT					. mrini	.												
61 (B) LOCATION: 1396 62 63 64 65 66 67 68 (XI) SEQUENCE DESCRIPTION: SEQ ID NO:1: 69 70 ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Trp Val Pro 1 5 10 15 73 74 GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT 61y Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala 76 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala 77 78 GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AAC AGT 79 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser 80 35 81 82 GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA 83 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 84 50 55 85 GGA CAG CCA CAA ACT CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT 88 GG ATC CCA AAC CCC AAA CTC CTC ATC TAT GCT GGA ACC ATC TCT AGC GLy Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 88 65 70 75 80 89 GGG ATC CCA ACC CAGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC 819 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 85 90 GCT CAAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT 86 CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT 97 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GCC ACC AAG CTG 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GCC ACC AAC CTG 97 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GCC ACC AAC CTG 97 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GCC ACC AAC CTG 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GCC ACC AAC CTG 97 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GCC ACC AAC CTG 97 98 00 01 01 01 01 01 01 01 01 01 01 01 01			(IX				ZEV.	CDG										
62 63 64 64 65 66 66 67 67 68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 69 70 ATG GAG ACA GAC ACC ATC CTA TGG GTG CTG CTG CTC TGG GTT CCA 68 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro 15 10 15 15 15 10 15 15 15 15 15 10 15 15 15 15 15 15 15 15 15 15 15 15 15				•	•				396									
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74 GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT 96 75 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala 30 76 20 25 30 77 GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT 144 79 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser 40 80 35 40 45 81 GTT GAT TAT GAT GGT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA 192 83 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 55 60 85 GGA CAG CCA CCC AAA CTC CTC ATC TTT TAT GCT GCA TCC AAT CTA GAA TCT 240 87 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 80 88 65 70 75 80 89 GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TTT GGG ACA GAC TTC ACC 288 91 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 95 93 94 CTC AAC ATC CAT CCT GTG GAG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT TYC Cys 105 110 96 CAG CAA AGT AAT GAG GAT CCT CCG ACG TC CCG ACG TTC CCG ACG T		_				3					10					15		
76		GGC	TCC	ACT	GGT	GAC	ATT	GTG	CTG	ACC	CAA	TCT	CCA	GCT	TCT	TTG	GCT	96
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84 50 55 55 60 85 85 86 GGA CAG CCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT 240 87 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 88 65 70 70 75 80 80 89 90 GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC 288 91 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 92 85 90 95 93 94 CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT 336 95 Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys 100 100 105 110 97 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG 384																		172
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90		65					70					75					80	
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93 94 CTC AAC ATC CAT CCT GTG GAG GAG GAT GCT GCA ACC TAT TAC TGT 336 95 Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys 96 100 105 110 97 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG 384		GTÀ	ITe	Pro	Ala	_	Phe	Ser	СТĀ	Ser	_	Ser	GTÀ	Thr	Asp		Thr	
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95 Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys 96 100 105 110 97 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG 384		CTC	אאמ	አሞር	CAT	CCT	стс	GNG	GVG	GVG	CAT	CCT	GCA	N.C.C	ייטעיים	ጥአር	ጥርጥ	336
96 100 105 110 97 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG 384																		330
97 98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG 384		Deu	NO!!	TT6		110	* 4.3.	- Lu	<u></u>		rsb	41.I.U	ALG		_	- 1 -	0,5	
98 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG 384																		
		CAG	CAA	AGT	AAT	GAG	GAT	CCT	CCG	ACG	TTC	GGT	GGA	GGC	ACC	AAG	CTG	384

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100			115					120					125					
101																		
102			AAA															396
103	Glu	Ile	Lys	Arg														
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107	(2)	INF	ORMA'	TION	FOR	SEO	ID 1	NO: 2	:									
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118		GIU	Thr	Asp		тте	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp		Pro		
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121	GTÄ	Ser	Thr	-	Asp	ITe	Val	Leu		Gln	Ser	Pro	Ala		Leu	Ala		
122				20					25					30				
123															_			
124	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser		
125			35					40					45					
126						•												
127	Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro		
128		50					55					60						
129																		
130																		
131	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser		
132	65				_	70			_		75					80		
133																		
134	Gly	Ile	Pro	Ala	Arq	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr		
135	-				85			-		90		-		_	95			
136																		
137	Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tvr	Tvr	Cvs		
138				100					105					110	- 2 -	-1-		
139																		
140	Gln	Gln	Ser	Asn	Glu	Asp	Pro	Pro	Thr	Phe	Glv	Glv	G1 v	Thr	Lvs	Leu		
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147	(2)	TNE.	UKMA'	rion	FOR	SEQ	ן מד	5:UK	:									
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149		(1		QUEN														
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153			(1	D) T(OPOL	OGY:	unk	nown									
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155		(ii) MO	LECU	LE T	YPE:	CDN	A									
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157		(ix) FE	ATUR	E:												
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159			(1	B) L	OCAT:	ION:	64.	.483									
160																	
161		(xi) SE	QUEN	CE D	ESCR:	IPTI(ON:	SEQ :	ID N	0:3:						
162																	
163	GAA'	rtcg	CGG (CCGC'	TATG	CA G	GGAC	AATC	A GC	AGCA	GCAA	TGA	GGAA(GTA A	AGCC'	rgtgca	. 60
164																	
165	GAT	ATG	AAC	AGG	CTT	ACT	TCC	TCA	TTG	CTG	CTG	CTG	ATT	GTC	CCT	GCA	108
166		Met	Asn	Arg	Leu	Thr	Ser	Ser	Leu	Leu	Leu	Leu	Ile	Val	Pro	Ala	
167		1				5					10					15	
168																	
169						GTT											156
170	Tyr	Val	Leu	Ser	Gln	Val	Thr	Leu	Lys	Glu	Ser	Gly	Pro	Gly	Ile	Leu	
171					20					25					30		
172																	
173						CTC											204
174	Gln	Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Phe	Ser	Gly	Phe	Ser	
175				35					40					45			
176																	
177	CTG	AGC	ACT	TCT	GGT	ATG	GGT	GTG	AGC	TGG	ATT	CGT	CAG	CCT	TCA	GGA	252
178	Leu	Ser	Thr	Ser	Gly	Met	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Ser	Gly	
179			50					55					60				
180																	
181	AAG	GGT	CTG	GAG	TGG	CTG	GCA	CAC	ATT	TAC	TGG	GAT	GAT	GAC	AAG	CGC	300
182	Lys	Gly	Leu	Glu	Trp	Leu	Ala	His	Ile	Tyr	Trp	Asp	Asp	Asp	Lys	Arg	
183		65					70					75					
184																	
185	TAT	AAC	CCA	TCC	CTG	AAG	AGC	CGG	CTC	ACA	ATC	TCC	AAG	GAT	ACC	TCC	348
186	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	
187	80					85					90					95	
188																	
189	AGC	AAC	CAG	GTA	TTC	CTC	AAG	ATC	ACC	AGT	GTG	GAC	ACT	GCA	GAT	ACT	396
190	Ser	Asn	Gln	Val	Phe	Leu	Lys	Ile	Thr	Ser	Val	Asp	Thr	Ala	Asp	Thr	
191					100					105					110		
192																	
193																	
194						GCT											444
195	Ala	Thr	Tyr	Tyr	Cys	Ala	Arg	Arg	Glu	Thr	Val	Phe	Tyr	Trp	Tyr	Phe	
196				115					120					125			
197																	
198						GGG											483
199	Asp	Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
200			130					135					140				
201																	
202																	
203	(2)	INF	ORMA	rion	FOR	SEQ	ID I	NO:4	:								
204																	
205		((i) S	SEQUE	ENCE	CHA	RACTI	ERIS	rics	:							

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/612,929

DATE: 03/06/97 TIME: 16:01:13

206 207 208 209	(A) LENGTH: 140 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear															
210 211		(:	ii) 1	MOLE	CULE	TYP	TYPE: protein									
212 213		(:	xi) :	SEQUI	ENCE	DES	DESCRIPTION: SEQ ID NO:4:									
214 215 216	Met 1	Asn	Arg	Leu	Thr 5	Ser	Ser	Leu	Leu	Leu 10	Leu	Ile	Val	Pro	Ala 15	Tyr
217 218 219	Val	Leu	Ser	Gln 20	Val	Thr	Leu	Lys	Glu 25	Ser	Gly	Pro	Gly	Ile 30	Leu	Gln
220 221	Pro	Ser	Gln 35	Thr	Leu	Ser	Leu	Thr 40	Cys	Ser	Phe	Ser	Gly 45	Phe	Ser	Leu
222 223 224	Ser	Thr 50	Ser	Gly	Met	Gly	Val 55	Ser	Trp	Ile	Arg	Gln 60	Pro	Ser	Gly	Lys
225 226 227 228	Gly 65	Leu	Glu	Trp	Leu	Ala 70	His	Ile	Tyr	Trp	Asp 75	Asp	Asp	Lys	Arg	Tyr 80
229 230 231	Asn	Pro	Ser	Leu	Lys 85	Ser	Arg	Leu	Thr	Ile 90	Ser	Lys	Asp	Thr	Ser 95	Ser
232 233 234	Asn	Gln	Val	Phe 100	Leu	Lys	Ile	Thr	Ser 105	Val	Asp	Thr	Ala	Asp 110	Thr	Ala
235 236 237	Thr	Tyr	Tyr 115	Cys	Ala	Arg	Arg	Glu 120	Thr	Val	Phe	Tyr	Trp 125	Tyr	Phe	Asp
238 239 240	Val	Trp 130	Gly	Ala	Gly	Thr	Thr 135	Val	Thr	Val	Ser	Ser 140				
241 242 243	(2)	INFO	ORMAT	rion	FOR	SEQ	ID 1	10:5	:							
244 245 246 247 248 249	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 60 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: unknown															
250 251		(ii) MOI	LECUI	LE TY	PE:	cDN/	A								
252 253 254 255 256		(ix)		A) N2	AME/I	KEY:	CDS 1	50								
257 258		(xi)) SE(QUENC	CE DE	ESCR	(PTIC	ON: S	SEQ I	D NO):5:					

PAGE: i

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/612,929

DATE: 03/06/97 TIME: 16:01:16

Line	Error	Original Text
30	Wrong application Serial Number	(A) APPLICATION NUMBER: US 08/117,366
34	Wrong application Serial Number	(A) APPLICATION NUMBER: US 08/136,783